

Db 181 ASDNQAILDSIGKLT SFDLLQALLOSVANNKKAELLKEMQDNDNPVVPFGKTPAIAQSLVD 240

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: March 23, 2004, 10:53:56 / Search time 17.7616 Seconds
(without alignments)
3525.629 Million cell updates/sec

Title: US-10-608-559-2

Perfect score: 3187

Sequence: 1 MNPVIGPGEIDERTPPAD.....SIFQCVLVNIGSLYSGTQ 651

Scoring table: BLOSUM62

Gapop 10.0 / Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2030000200

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3187	100.0	651	D72042	conserved hypophet
2	3187	100.0	651	B8581	CHUPN 76 kDa homol
3	2205	69.2	715	I40729	hypothetical 76K P
4	899.5	28.2	647	G71490	hypothetical prote
5	233.5	7.3	2055	T31110	extracellular matr
6	232	7.3	1822	S33441	EF protein - Strept
7	223.5	7.0	2481	D90011	Fmcb protein (Impo
8	221.5	7.0	971	B90835	probable tail fibre
9	221.5	7.0	971	C85693	probable membrane
10	220	6.9	6713	B89921	hypothetical prote
11	210	6.6	1122	G64887	probable tail fibre
12	210	6.6	2271	P90073	hypothetical prote
13	208.5	6.5	4776	E95206	cell wall surface
14	199	6.2	1365	T30822	Impi protein - Myc
15	196.5	6.2	1829	T24583	hypothetical prote
16	196.5	6.2	2232	T34434	hypothetical prote
17	192	6.0	1156	T34852	probable secreted
18	190.5	6.0	1063	D66731	hypothetical prote
19	189	5.9	2155	AD2742	conserved hypophet
20	189	5.9	2155	C97523	hypothetical prote
21	187	5.9	1147	T15781	hypothetical prote
22	186.5	5.9	1306	S25370	hypothetical prote
23	183	5.7	2186	H89960	MS2 protein - Yea
24	182.5	5.7	641	C82206	methy-accepting c
25	182.5	5.7	1238	T03465	probable exonuclea
26	182.5	5.7	2541	S11661	tailin - mouse
27	182	5.7	1269	F84730	probable myosin he
28	178.5	5.6	1566	A43607	cell surface antigen
29	177	5.6	2090	S26058	probable transform

10	176.5	5.5	545	2	E84327	Hrr7 transducer [1
31	176.5	5.5	545	2	T46811	halobacterial tran
32	176.5	5.5	3890	2	C89921	hypothetical prote
33	175.5	5.5	1104	2	S59310	probable membrane
34	175.5	5.5	5327	2	T13564	microtubule-associ
35	175	5.5	627	2	F84194	Hrr14 transducer [
36	175	5.5	891	2	G41662	130K surface exclu
37	175	5.5	1302	1	JC6009	surface-located me
38	173.5	5.4	1561	1	S06839	surface antigen sp
39	173	5.4	1072	2	A86827	hypothetical prote
40	173	5.4	2285	2	T12796	probable transglyc
41	172.5	5.4	1128	2	T30296	R27-2 protein - Tr
42	172.5	5.4	1601	2	AB1730	hypothetical prote
43	171.5	5.4	990	2	T51618	nucleolar phosphop
44	171	5.4	1787	2	AG1360	probable tape-meas
45	170.5	5.3	583	2	S67571	hypothetical prote

ALIGNMENTS

RESULT 1
D72042
conserved hypothetical protein CP0018 [imported] - Chlamydia pneumoniae (strains CM
N/Altemate names: chlpn 76 kDa homolog 1 (c622); hypothetical protein CP00728
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C/Accession: D72042, D81623
R/Kalman, S.; Mitchell, W.; Marathe, R.; Jammal, C.; Fan, J.; Olinger, L.; Grimwood, J.
Nucleic Acids Res. 21, 385-389, 1999

A/Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A/Reference number: A72000; PMID:9206606; PMID:10192388
A/Accession: D72042
A/Molecule type: DNA

A/Residues: 1-651 <RNA>
A/Cross-references: GB:AE001654; GB:AE001363; NID:94377031; EIDN:AD01867.1; PID:943770.
A/Experimental source: Strain CM029
R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hick
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salz
Nucleic Acids Res. 28, 1397-1406, 2000

A/Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR3
A/Reference number: AB1500; PMID:20150255; PMID:10664935
A/Accession: D81623
A/Status: Preliminary
A/Molecule type: DNA

A/Residues: 1-651 <RNA>
A/Cross-references: GB:AE002165; GB:AE002161; NID:97188948; PIDN:AE37914.1; PID:971889.
A/Experimental source: strain AR35, HL cells
C/Comment: This sequence was originally identified as homologous to part of a sequence
C/Genetics: PIR:H71490.

A/Gene: CP00728; CP0018
Query Match
Best Local Similarity 100.0%; Score 3187; DB 2; Length 651;
Matches 651; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	MNPVIGPGEIDERTPPADLSAOGLESAANKSAEORIGAEKPKSTDSVERSI	60
QY	61	LRSAVNAISADKLGTAASNSSTSRADVDSTTAAPPPPTDQYKQAYDT	120
DB	61	LRSAVNAISADKLGTAASNSSTSRADVDSTTAAPPPPTDQYKQAYDT	120
QY	121	IFSTSLADIQAALVSIQDAVTNKTAAATDETAIAEMETKNADAVKVAQTTELAKY	180
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 DB 241 QTDATATCTEKGNAIRDAVYFAGONASGAVENAKSNNSISINDSAKAAATATKTOIAEAO 300
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 DB 361 DDENETATILMSGRQWIMHNTENPDSQAQCELAQAQAADGDSAAALADAK 420
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 DB 481 QISAGDAKSIINDAGRAKNDATRDVNNVSTPALTRSPRATKTEARGEKTDALARY 540
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 DB 481 QISAGDAKSIINDAGRAKNDATRDVNNVSTPALTRSPRATKTEARGEKTDALARY 540
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 DB 541 ISGNSRTIGDYVSQVSAQSVMQIISNPQANNEIRKQLSAVTKPQFGYFYQLSND 600
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 DB 541 ISGNSRTIGDYVSQVSAQSVMQIISNPQANNEIRKQLSAVTKPQFGYFYQLSND 600
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 DB 601 STOKFIKESLFAEGSRFAEIKALSFETNSLFIQVNVNIGSLYSGYLQ 651

RESULT 2

28581
 CHLBN 76 kDa homolog 1 (C7622) [imported] - Chlamydia pneumoniae (strain J138)
 C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
 C:Accession: B86581
 R:Shirai, M.; Hiraoka, H.; Kimoto, M.; Tachuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Iw
 Nucleic Acids Res. 28, 2311-2314, 2000
 A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
 A:Reference number: A86491; PMID:20390349; PMID:10811362
 A:Accession: B86581
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-651 <STO>
 A:Cross-references: GB:BA000008; NID:58979100; PID:BA98935.1; GSDB:GN0142
 A:Experimental source: strain J138
 A:Genetics:
 A:Gene: CP10728

Query Match 100.0%; Score 3187; DB 2; Length 651;
 Best Local Similarity 100.0%; Pred. No. 1.9e-146; Indels 0; Gaps 0;
 Matches 651; Conservative 0; Mismatches 0;

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 DB 121 IFTSTSLADICALLVSLQDAVTNIKOTAAIDEETALAEWEKNDAYVGAQITELAKY 180
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 DB 241 QTDATATCTEKGNAIRDAVYFAGONASGAVENAKSNNSISINDSAKAAATATKTOIAEAO 300
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RESULT 3

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 hypothetical 76k protein - Chlamydia pneumoniae (strain AF39)
 C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
 C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 31-Mar-2000
 C:Accession: Z40728
 R:Peretz-Melgosa, M.; Kuo, C.
 Infect. Immun. 62, 880-886, 1994
 A:Title: Isolation and characterization of a gene encoding a Chlamydia pneumoniae 76-kD
 A:Reference number: 140729; PMID:94156481; PMID:7509320
 A:Accession: Z40728
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-715 <RES>
 A:Cross-references: GB:U23921; NID:9435961; PID:AAA23117.1; PID:9435962
 A:Experimental source: strain AF-39
 A:Comment: This is the hypothetical translation of a sequence that was reported as two

Query Match 99.6%; Score 2205; DB 2; Length 715;
 Best Local Similarity 99.6%; Pred. No. 1.9e-100; Indels 0; Gaps 0;
 Matches 452; Conservative 1; Mismatches 1;

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 DB 1 MNPIGPGPIDEETERTPPADLSAQLIEMSAANKSAEORIGAEKPEKSTDSVERKSI 60
 QY 61 IRSVNAALMSLADKLGIASSNSSSTSRADVSTTATPPTPTFDYKTOAQIAYDT 120
 DB 61 IRSVNAALMSLADKLGIASSNSSSTSRADVSTTATPPTPTFDYKTOAQIAYDT 120
 QY 121 IFTSTSLADICALLVSLQDAVTNIKOTAAIDEETALAEWEKNDAYVGAQITELAKY 180
 DB 121 IFTSTSLADICALLVSLQDAVTNIKOTAAIDEETALAEWEKNDAYVGAQITELAKY 180
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 DB 181 ASDNQAALIDSLGKTSFDLQALLOSVAANNKAAELKEMQNPVVPKTPALIAQSLVD 240
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 DB 421 ALEALAGKAGQOQGIINLALQIASAAVYAGVPPAAASISGSSVKOLYKTSKTSQDYKT 480
 QY 481 QISAGDAKSIINDAGRAKNDATRDVNNVSTPALTRSPRATKTEARGEKTDALARY 540
 DB 481 QISAGDAKSIINDAGRAKNDATRDVNNVSTPALTRSPRATKTEARGEKTDALARY 540
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LOCUS amylin pneumoniae section 76 of 103 of the complete genome.
10421 bp DNA linear BCT 01-DEC-2000
10421 bp DNA linear BCT 01-DEC-2000
10421 bp DNA linear BCT 01-DEC-2000

REFERENCE
1 (bases 1 to 10421)
Kalmann, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Hyman, R. W.,
Olinger, L., Grimwood, J., Davis, R. W., and Stephens, R. S.
Comparative genomes of Chlamydia pneumoniae and C. trachomatis
Nat. Genet. 21 (4), 385-389 (1999)

JOURNAL
MEDLINE
PUBMED
10192388
2 (bases 1 to 10421)
Kalmann, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Olinger, L.,
Grimwood, J., Davis, R. W., and Stephens, R. S.
Direct Submision
Submitted (01-DEC-1998) Program in Infectious Diseases, University
of California, 235 Earl Warren Hall, Berkeley, CA 94720, USA

AUTHORS
TITLE
JOURNAL
SUBMITTER
LOCATION/Qualifiers
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2101 AAGGCTTGTGAGGCTTCAACCAACACTAGACGATCTCAATTAATTAAGA 2156
2101 AAGGCTTGTGAGGCTTCAACCAACACTAGACGATCTCAATTAATTAAGA 2156

RESULT 2
AE001654/c 10421 bp DNA linear BCT 01-DEC-2000
LOCUS amylin pneumoniae section 76 of 103 of the complete genome.
10421 bp DNA linear BCT 01-DEC-2000
10421 bp DNA linear BCT 01-DEC-2000
10421 bp DNA linear BCT 01-DEC-2000

REFERENCE
1 (bases 1 to 10421)
Kalmann, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Hyman, R. W.,
Olinger, L., Grimwood, J., Davis, R. W., and Stephens, R. S.
Comparative genomes of Chlamydia pneumoniae and C. trachomatis
Nat. Genet. 21 (4), 385-389 (1999)

JOURNAL
MEDLINE
PUBMED
10192388
2 (bases 1 to 10421)
Kalmann, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Olinger, L.,
Grimwood, J., Davis, R. W., and Stephens, R. S.
Direct Submision
Submitted (01-DEC-1998) Program in Infectious Diseases, University
of California, 235 Earl Warren Hall, Berkeley, CA 94720, USA

AUTHORS
TITLE
JOURNAL
SUBMITTER
LOCATION/Qualifiers
1. 10421
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